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RAW SEQUENCE LISTING

DATE: 09/24/2002

PATENT APPLICATION: US/09/980,881A

TIME: 13:41:28

Input Set : N:\Crf4\09122002\I980881.raw

Output Set: N:\CRF4\09242002\I980881A.raw

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1 <110> APPLICANT: AKIRA MATSUMOTO
2 <120> TITLE OF INVENTION: Human Brain Carboxypeptidase B
3 <130> FILE REFERENCE: MAT-101PCT
4 <140> CURRENT APPLICATION NUMBER: US/09/980,881A
5 <141> CURRENT FILING DATE: 2001-10-30
6 <150> PRIOR APPLICATION NUMBER: JP 1999-125169
7 <151> PRIOR FILING DATE: 1999-04-30
8 <160> NUMBER OF SEQ ID NOS: 9
9 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1573
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (18)..(1097)
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20                      Met Lys Leu Cys Ser Leu Ala Val Leu Val Pro
21                      1                      5                      10
22      att gtt ctc ttc tgt gag cag cat gtc ttc gcg ttc cag agt ggc caa      98
23      Ile Val Leu Phe Cys Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln
24                      15                      20                      25
25      gtt cta gct gct ctt cct aga acc tct agg caa gtt caa gtt cta cag      146
26      Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln
27                      30                      35                      40
28      aat ctt act aca aca tat gag att gtt ctc tgg cag ccg gta aca gct      194
29      Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala
30                      45                      50                      55
31      gac ctt att gtg aag aaa aaa caa gtc cat ttt ttt gta aat gca tct      242
32      Asp Leu Ile Val Lys Lys Lys Gln Val His Phe Phe Val Asn Ala Ser
33                      60                      65                      70                      75
34      gat gtc gac aat gtg aaa gcc cat tta aat gtg agc gga att cca tgc      290
35      Asp Val Asp Asn Val Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys
36                      80                      85                      90
37      agt gtc ttg ctg gca gac gtg gaa gat ctt att caa cag cag att tcc      338
38      Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser
39                      95                      100                      105
40      aac gac aca gtc agc ccc cga gcc tcc gca tcg tac tat gaa cag tat      386
41      Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr
42                      110                      115                      120
43      cac tca cta aat gaa atc tat tct tgg ata gaa ttt ata act gag agg      434
44      His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg
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45	125	130	135	
46	cat cct gat atg ctt aca aaa atc cac att gga tcc tca ttt gag aag	482		
47	His Pro Asp Met Leu Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys			
48	140	145	150	155
49	tac cca ctc tat gtt tta aag gtt tct gga aaa gaa caa aca gcc aaa	530		
50	Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys			
51	160	165	170	
52	aat gcc ata tgg att gac tgt gga atc cat gcc aga gaa tgg atc tct	578		
53	Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser			
54	175	180	185	
55	cct gct ttc tgc ttg tgg ttc ata ggc cat aat cga atg tgg aga aag	626		
56	Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys			
57	190	195	200	
58	aac cgt tct ttc tat gcg aac aat cat tgc atc gga aca gac ctg aat	674		
59	Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn			
60	205	210	215	
61	agc aac ttt gtc tcc aaa cac tgg tgt gag gaa ggt gca tcc agt tcc	722		
62	Ser Asn Phe Val Ser Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser			
63	220	225	230	235
64	tca tgc tcg gaa acc tac tgt gga ctt tat cct gag tca gaa cca gaa	770		
65	Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu			
66	240	245	250	
67	gtg aag gca gtg gct agt ttc ttg aga aga aat atc aac cag att aaa	818		
68	Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys			
69	255	260	265	
70	gca tac atc agc atg cat tca tac tcc cag cat ata gtg ttt cca tat	866		
71	Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr			
72	270	275	280	
73	tcc tat aca cga agt aaa agc aaa gac cat gag gaa ctg tct cta gta	914		
74	Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val			
75	285	290	295	
76	gcc agt gaa gca gtt cgt gct att gac aaa act agt aaa aat acc agg	962		
77	Ala Ser Glu Ala Val Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg			
78	300	305	310	315
79	tat aca cat ggc cat ggc tca gaa acc tta tac cta gct cct gga ggt	1010		
80	Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly			
81	320	325	330	
82	ggg gac gat tgg atc tat gat ttg ggc atc aaa tat tcg ttt aca tca	1058		
83	Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser			
84	335	340	345	
85	aac cca cct gta gag aag ctt ttg ccg ctg tct cta aaa tagcttgga	1107		
86	Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser Leu Lys			
87	350	355	360	
88	tgctcattagg aatgtttaat gcccctgatt ttatcattct gcttccgtat ttttaatttac	1167		
89	tgattccagc aagaccaaatt cattgtatca gattattttt aagttttatc cgtagttttg	1227		
90	ataaaagatt ttcctattcc ttggttctgt cagagaacct aataagtgt actttgcca	1287		
91	taaggcagac tagggttcat gtctttttac cctttaaaaa aaaattgtaa aagcttagtt	1347		
92	acctactttt tctttgattt tcgacgtttg actagccatc tcaagcaact ttcgacgttt	1407		
93	gactagccat ctcaagcaag tttaaatcaaa gatcatctca cgctgatcat tggatcctac	1467		

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94      tcaacaaaag gaaggggtggt cagaagtaca ttaaagattt ctgctccaaa ttttcaataa 1527
95      atttcttctt ctccttttaa aaaaaaaaaa aaaaaaaaaa aaaaaa      1573
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 360
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 2
102      Met Lys Leu Cys Ser Leu Ala Val Leu Val Pro Ile Val Leu Phe Cys
103      1          5          10          15
104      Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln Val Leu Ala Ala Leu
105      20          25          30
106      Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln Asn Leu Thr Thr Thr
107      35          40          45
108      Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala Asp Leu Ile Val Lys
109      50          55          60
110      Lys Lys Gln Val His Phe Phe Val Asn Ala Ser Asp Val Asp Asn Val
111      65          70          75          80
112      Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys Ser Val Leu Leu Ala
113      85          90          95
114      Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser Asn Asp Thr Val Ser
115      100         105         110
116      Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu
117      115         120         125
118      Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu
119      130         135         140
120      Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val
121      145         150         155         160
122      Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile
123      165         170         175
124      Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu
125      180         185         190
126      Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr
127      195         200         205
128      Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn Ser Asn Phe Val Ser
129      210         215         220
130      Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr
131      225         230         235         240
132      Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala
133      245         250         255
134      Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met
135      260         265         270
136      His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser
137      275         280         285
138      Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val
139      290         295         300
140      Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His
141      305         310         315         320
142      Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile
143      325         330         335

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144      Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu
145                      340                      345                      350
146      Lys Leu Leu Pro Leu Ser Leu Lys
147                      355                      360
149 <210> SEQ ID NO: 3
150 <211> LENGTH: 338
151 <212> TYPE: PRT
152 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 3
154      Phe Gln Ser Gly Gln Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln
155      1                      5                      10                      15
156      Val Gln Val Leu Gln Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp
157                      20                      25                      30
158      Gln Pro Val Thr Ala Asp Leu Ile Val Lys Lys Lys Gln Val His Phe
159                      35                      40                      45
160      Phe Val Asn Ala Ser Asp Val Asp Asn Val Lys Ala His Leu Asn Val
161                      50                      55                      60
162      Ser Gly Ile Pro Cys Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile
163                      65                      70                      75                      80
164      Gln Gln Gln Ile Ser Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser
165                      85                      90                      95
166      Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu
167                      100                     105                     110
168      Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys Ile His Ile Gly
169                      115                     120                     125
170      Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys
171                      130                     135                     140
172      Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala
173                      145                     150                     155                     160
174      Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn
175                      165                     170                     175
176      Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile
177                      180                     185                     190
178      Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His Trp Cys Glu Glu
179                      195                     200                     205
180      Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro
181                      210                     215                     220
182      Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn
183                      225                     230                     235                     240
184      Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His
185                      245                     250                     255
186      Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu
187                      260                     265                     270
188      Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala Ile Glu Lys Thr
189                      275                     280                     285
190      Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr
191                      290                     295                     300
192      Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys
193                      305                     310                     315                     320

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194      Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser
195                      325                      330                      335
196      Leu Lys
198 <210> SEQ ID NO: 4
199 <211> LENGTH: 246
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 4
203      Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr
204          1                      5                      10                      15
205      Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys
206                      20                      25                      30
207      Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys
208                      35                      40                      45
209      Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys
210          50                      55                      60
211      Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe
212          65                      70                      75                      80
213      Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn
214                      85                      90                      95
215      Asn His Cys Ile Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His
216                      100                      105                      110
217      Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys
218          115                      120                      125
219      Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe
220          130                      135                      140
221      Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser
222          145                      150                      155                      160
223      Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser
224                      165                      170                      175
225      Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala
226                      180                      185                      190
227      Ile Glu Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser
228                      195                      200                      205
229      Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp
230          210                      215                      220
231      Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu
232          225                      230                      235                      240
233      Leu Pro Leu Ser Leu Lys
234                      245
236 <210> SEQ ID NO: 5
237 <211> LENGTH: 24
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
242      synthesized oligopeptide sequence
243 <400> SEQUENCE: 5
244      Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu

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VERIFICATION SUMMARY

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